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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2618.26 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-2
Perfect score: 1017
Sequence: 1 atgaagtttattactattgc.....caggttgttcaagaaaataa 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	217.4	21.4	808	3	AB045178	AB045178 Reticulit
2	217.4	21.4	828	3	AB045179	AB045179 Reticulit
3	214.2	21.1	840	3	AB045172	AB045172 Reticulit
4	211.8	20.8	710	3	AB045171	AB045171 Reticulit
5	208.4	20.5	774	3	AB045170	AB045170 Reticulit
6	204	20.1	780	3	AB045168	AB045168 Reticulit
7	198.8	19.5	784	3	AB045167	AB045167 Reticulit
8	196.4	19.3	781	3	AB045165	AB045165 Reticulit
9	194.8	19.2	785	3	AB045177	AB045177 Reticulit
10	194.4	19.1	759	3	AB045174	AB045174 Reticulit
11	192.6	18.9	783	3	AB045173	AB045173 Reticulit
12	191.2	18.8	802	3	AB045176	AB045176 Reticulit
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16	189.4	18.6	1473	6	A23646	A23646 F. oxysporu
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22	189.4	18.6	1473	6	BD010853	BD010853 Cellulase
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24	189.4	18.6	1473	6	I21317	I21317 Sequence 3
25	189.4	18.6	1473	6	I57984	I57984 Sequence 3
26	188.4	18.5	761	3	AB045175	AB045175 Reticulit
27	187.6	18.4	798	3	AB045166	AB045166 Reticulit
28	186.2	18.3	785	3	AB045169	AB045169 Reticulit
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31	181	17.8	960	6	AR094305	AR094305 Sequence
32	180.8	17.8	919	6	A68072	A68072 Sequence 67
33	180.8	17.8	919	6	AR163168	AR163168 Sequence
34	180	17.7	894	6	AR094306	AR094306 Sequence
35	178.8	17.6	924	6	A68074	A68074 Sequence 69
36	178.8	17.6	924	6	AR163169	AR163169 Sequence
37	173.8	17.1	1132	6	AR094315	AR094315 Sequence
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39	169.6	16.7	922	6	A68070	A68070 Sequence 65
40	169.6	16.7	922	6	AR163167	AR163167 Sequence
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43	160.4	15.8	885	6	AR094316	AR094316 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AB045178 808 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:45-6, complete cds.
ACCESSION AB045178
VERSION AB045178.1 GI:8926988
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:45-6.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family

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            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 808)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
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  Best Local Similarity   62.1%;  Pred. No. 6.9e-50;
  Matches  382;  Conservative    0;  Mismatches  221;  Indels   12;  Gaps    2;

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Db         88 ACAACTCGCTATTGGGATTGTTGTAAGGGGAGCTGTGGATGGGATGGCAAGGCTTCCGTG 147

Qy        463 AGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTTAGTGACAGCAATGCC 522
              || ||  |  | |||   ||||||||     |||    ||     |||
Db        148 TCCAAGCCCGTTGACACATGTGCAAAAGATGGAACAACTCGAGTTGCAACCAGCGCAAAA 207

Qy        523 CAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAACCTTGGGCTGTA 582
              |  | ||  ||  || || |     || ||||||| | ||  |   |||  | |||||
Db        208 TCAGCTTGCGATAGTGGCGGCACAGCATATATGTGTTATGATCAAACACCGCGTGCTGTC 267

Qy        583 AACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGC 642
              || ||      ||||  ||| || |||||||| ||  |    |||||||   || |
Db        268 AATGATTCATATGCCATTGGGTTTGCTGCTGCGGCTGTTTCAGGTGGTGAGAAAGC---G 324

Qy        643 TGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATG 702
              ||||||| | |||| |||||| ||||||||||||  | |||||  ||| |||||||||
Db        325 GCGTGCTGTACGTGTTACGAACTCACTTTCACTTCTGGCCCTGTTAATGGAAAGAAGATG 384

Qy        703 GTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTTGAC 762
              ||| ||||| || || || || |||||||||||| |||          ||| |||||
Db        385 ACTGTTCAAGTGACCAATACGGGAGGTGATCTTGGTTCC---------AATCAATTTGAT 435

Qy        763 TTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGTTCCAGCCAATGGGGTGCT 822
              |    || ||||| || |||||||||  ||| ||| |||||  |     |||| ||||||
Db        436 ATTGCGATTCCCGGCGGAGGTGTTGGACTTTACAACGGTTGCACTTCTCAATCGGGTGCA 495

Qy        823 CCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGT 882
              ||    || || |||||     |||| || ||| |||| |||  |  ||| || |||
Db        496 CCTGCAGATGGATGGGGAAGCCGATATGGAGGTGTTTCCTCTCGAAGTGAGTGTTCTCAG 555

Qy        883 CTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCTGAT 942
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Db        556 CTTCCTTCTGGTCTTCAAGCCGGGTGCCAGTGGCGTTTTGACTGGTTCCAAAATGCTGAT 615

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Db        616 AATCCGTCAATTACATTCAACGAAGTGAGTTGTCCAGGTGACTTGACAAGCAAAACCAAT 675

Qy       1003 TGTTCAAGAAAATAA 1017
              ||   | |  | |||
Db        676 TGCAGACGCCAGTAA 690


RESULT 2
AB045179
LOCUS       AB045179                828 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:6-47, complete cds.
ACCESSION   AB045179
VERSION     AB045179.1  GI:8926990
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:6-47.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 828)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
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Db         73 TGATTCTGGGAGGACTACGCGTTATTGGGATTGTTGCAAAGCGTCATGTGCATGGGAAAA 132

Qy        450 TAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT-- 507
              || ||   ||| | |  |||||  |  | |||   ||||||||    ||    |||
Db        133 AAAAGCTGCTGTGACTCAGCCTGTTGATACGTGTGGAAAAGATGGGACAACAAGACTTGC 192

Qy        508 -AGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAA 566
               || |  ||  |   ||   | ||| | || ||  |  | |||||||| | ||  |
Db        193 AAGCAATGACACAGTAAAATCGAGTTGTGATGGCGGAGATGGATACATGTGTTATGATCA 252

Qy        567 CCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGG 626
              ||| |||||||| || |||    ||||||||||||| || ||||| ||    |  |
Db        253 AGCACCATGGGCTGTTAATGACTCAGTTGCCTATGGTTTTGCAGCTGCAGC---TTGCTG 309

Qy        627 TGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGT 686
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RESULT 3
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DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
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ACCESSION   AB045172
VERSION     AB045172.1  GI:8926976
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
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  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
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REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 840)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
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  Best Local Similarity   62.3%;  Pred. No. 5.5e-49;
  Matches  393;  Conservative    0;  Mismatches  223;  Indels   15;  Gaps    3;

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Db         72 TGATTCTGGGAGGACCACGCGTTACTGGGACTGTTGCAAAGCTTCGTGTGCATGGGAAAA 131

Qy        450 TAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT-- 507

Db        132 AAAAGCTGCTGTGACTCAGCCTGTTGACACATGCGCAAAAGATGGCACAACCAGAGTTGC 191

Qy        508 -AGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAA 566

Db        192 AAGCAATGACACAGTGAAATCTTGCTGTGATGGTGGAGAGGGATACATGTGTTATGATCA 251

Qy        567 CCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGG 626

Db        252 AGCACCTTGGGCTGTTAATGACTCGGTTGCATACGGTTTTGCCGCTGCAGC---TTGCTG 308

Qy        627 TGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGT 686

Db        309 TGGAGGCGAAAGCGGTGCTTGTTGCAATTGCTATGAGCTTACCTTCACCAGTGGCCCAGT 368

Qy        687 TGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTAC 746

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Qy        987 CACCGCCAAGACAGGTTGTTCAAGAAAATAA 1017

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RESULT 4
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LOCUS       AB045171                 710 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:7-50, complete cds.
ACCESSION   AB045171
VERSION     AB045171.1  GI:8926974
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:7-50.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 710)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
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(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)

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Qy        511 GACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAA 570
Db        185 AATGACACTGTGAAATCAGCTTGTGATGGTGGAGAAGGATATATGTGTTATGATCAAGCA 244

Qy        571 CCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGTGGT 630
Db        245 CCATGGGCAGTTAATGACTCTGTTGCGTACGGTTTTGCTGCTGCAGC---TTGCTGTGGG 301

Qy        631 GGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCT 690
Db        302 GGCGAAAGCGGAGCTTGCTGCAATTGCTATGAGCTTACATTCACAAGTGGACCAGTGAAT 361

Qy        691 GGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGT 750
Db        362 GGAAAGAAGATGGTTGTACAAGTCACCAACACCGGTGGTGATCTTGGCTCGAA------- 414

Qy        751 GCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGTTCCAGC 810
Db        415 --TCAGTTTGATCTTGCGATTCCGGGTGGAGGTGTTGGGATCTACAACGGTTGCACCCAG 472

Qy        811 CAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCTGCATCT 870
Db        473 CAATCAGGTGCACCTGCTGATGGATGGGGAAGCCGATATGGAGGTGTTTCATCCCGCAGC 532

Qy        871 GACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTC 930
Db        533 GAATGCTCTCAGCTTCCGTCGGGCCTTCAAGCTGGGTGCCAATGGAGATTTGATTGGTTC 592

Qy        931 AAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTAAGGAAATCACC 990
Db        593 CAAAATGCCGATAACCCTTCAATCAATTTCAACCAAGTGACATGCCCTGGTGAGTTAACG 652

Qy        991 GCCAAGACAGGTTGTTCAAGAAAATAA 1017
Db        653 GCAAAAACCAATTGCAAGCGCACTTAA 679
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RESULT 5
AB045170
LOCUS AB045170 774 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:8-38, complete cds.
ACCESSION AB045170
VERSION AB045170.1 GI:8926972
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-38.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
JOURNAL Extremophiles 4 (6), 343-349 (2000)
MEDLINE 21020023
REFERENCE 2 (bases 1 to 774)
AUTHORS Ohkuma,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

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FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="Reticulitermes speratus hindgut symbiont
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                     /clone="8-38"
     CDS             52. .714
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                     /product="family 45 cellulase homologue"
                     /protein_id="BAA98040.1"
                     /db_xref="GI:8926973"
                     /translation="MLAFVITLFLASVFGDTGRTTRYWDCCKGSCGWEKKANVDKPID
                     TCAKDGTTRVASNDTVKSGCDGGDGYMCYDQSPWGVNDSFALGFAAAAVSGGESAACC
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                     WGSRYGGVSSRSECCQLPSGLQAGCQWRFDWFQNADNPSISFNVVSCPSELIAKTNCR
                     RV"
BASE COUNT      179 a    144 c    212 g    239 t
ORIGIN
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Query Match 20.5%; Score 208.4; DB 3; Length 774;
Best Local Similarity 61.7%; Pred. No. 2.4e-47;
Matches 389; Conservative 0; Mismatches 226; Indels 15; Gaps 3;

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Qy        391 GGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGT 450
Db         97 GATACTGGCAGAACAACCCGTTATTGGGATTGCTGCAAAGGAAGTTGTGGCTGGGAGAAG 156

Qy        451 AAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT--- 507
Db        157 AAGGCTAATGTGGACAAGCCTATTGATACGTGCGCAAAAGATGGTACCACCAGAGTTGCA 216

Qy        508 AGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAAC 567
Db        217 AGCAACGACACCGTTAAGTCAGGCTGTGATGGCGGAGATGGATATATGTGTTATGATCAA 276

Qy        568 CAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGT 627
Db        277 TCTCCGTGGGGTGTCAATGATTCTTTTGCTCTGGGTTTTGCTGCTGCAGCGGTTTCAGGA 336

Qy        628 GGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTT 687
Db        337 GGTGAGAGCGCTGCC---TGCTGCAATTGTTACGAGTTAACATTCACTTCTGGCCCAGTT 393

Qy        688 GCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACT 747
Db        394 AATGGAAAGAAGATGACTGTTCAGGTTACCAACACTGGGGGTGACCTTGGTTCC------ 447

Qy        748 GGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGTTCC 807
Db        448 ---AATCAGTTTGATCTTGCCATTCCAGGTGGTGGTGTTGGAATCTACAACGGCTGTACC 504
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Qy        808 AGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCTGCA 867
Db        505 GCTCAATCTGGTGCTCCTGCTGATGGATGGGGAAGTCGTTATGGTGGTGTTTCCTCCCGA 564

Qy        868 TCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGG 927
Db        565 AGTGAATGCTGTCAGCTTCCGTCGGGACTTCAGGCTGGCTGCCAGTGGCGTTTTGACTGG 624

Qy        928 TTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTAAGGAAATC 987
Db        625 TTCCAGAACGCTGATAATCCGTCAATCAGCTTCAACGTGGTTTCGTGTCCTAGTGAGTTG 684

Qy        988 ACCGCCAAGACAGGTTGTTCAAGAAAATAA 1017
Db        685 ATTGCGAAAACGAACTGTAGACGTGTTTAA 714


RESULT 6
AB045168
LOCUS       AB045168                780 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:4-44, complete cds.
ACCESSION   AB045168
VERSION     AB045168.1  GI:8926968
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:4-44.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 780)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Reticulitermes speratus hindgut symbiont
                     130484"
                     /clone="4-44"
     CDS             31. .684
                     /codon_start=1
                     /product="family 45 cellulase homologue"
                     /protein_id="BAA98038.1"
                     /db_xref="GI:8926969"
                     /translation="MLVFVFLASAFCDSGKTTRYWDCCKGSCGWEAKADVSKPIDTCA
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                     ELTFTSGPVNGKKMTVQVTNTGGDLGSNQFDLAIPGGGVGIYNGCTAQSGAPADGWGS
                     RYGGVSSRSECSQLPSGLQAGCQWRFDWFQNADNPSMNFNVVSCPSELIAKTNCRRN"
BASE COUNT      196 a    155 c    206 g    223 t
ORIGIN

  Query Match         20.1%;  Score 204;  DB 3;  Length 780;
  Best Local Similarity   61.2%;  Pred. No. 4.1e-46;
  Matches  387;  Conservative    0;  Mismatches  230;  Indels   15;  Gaps    3;

Qy        388 TCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCC 447
Db         64 TGTGACAGTGGCAAAACGACCCGCTATTGGGACTGCTGCAAAGGCTCCTGTGGCTGGGAA 123

Qy        448 GGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT 507
Db        124 GCCAAAGCTGATGTCAGCAAACCGATAGACACGTGCGCAAAAGATGGCACAACTCGAGTT 183

Qy        508 AGTGACAGCAATGCCCAAAG---TGGCTGTAACGGTGGTAACAGTTACATGTGTAACGAC 564
Db        184 GCAAGCAACGATACAGTAAAATCTGGTTGTGATGGCGGTGACGGCTTCATGTGCTACGAT 243

Qy        565 AACCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGT 624
Db        244 CAAACCCCGTGGGGCGTCAACGATTCTTACGCGTTGGGATTTGCTGCTGCAGCAATTTCA 303

Qy        625 GGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCT 684
Db        304 GGAGGTGAGAAGGCTGCC---TGCTGTAATTGTTACGAGTTGACTTTCACCTCTGGCCCC 360

Qy        685 GTTGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCT 744
Db        361 GTTAATGGCAAGAAGATGACTGTTCAGGTTACCAACACCGGAGGTGATCTCGGTTC---- 416

Qy        745 ACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGT 804
Db        417 -----GAATCAATTTGATCTCGCCATTCCAGGTGGTGGTGTCGGTATTTACAATGGATGC 471

Qy        805 TCCAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCT 864
Db        472 ACAGCTCAATCTGGTGCTCCTGCTGATGGTTGGGGAAGTCGGTATGGAGGGGTCTCCTCC 531

Qy        865 GCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAAC 924
Db        532 CGCAGTGAATGCTCCCAGCTTCCTTCGGGTCTTCAGGCTGGCTGCCAGTGGAGATTCGAT 591

Qy        925 TGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTAAGGAA 984
Db        592 TGGTTCCAAAATGCCGACAATCCGTCCATGAACTTTAACGTCGTGTCGTGCCCCAGTGAG 651

Qy        985 ATCACCGCCAAGACAGGTTGTTCAAGAAAATA 1016
Db        652 TTGATTGCAAAAACCAATTGCAGACGCAATTA 683


RESULT 7
AB045167
LOCUS       AB045167                784 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:8-16, complete cds.
ACCESSION   AB045167
VERSION     AB045167.1  GI:8926966
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:8-16.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 784)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
     source          1. .784
                     /organism="Reticulitermes speratus hindgut symbiont
                     130484"
                     /clone="8-16"
     CDS             28. .690
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                     /db_xref="GI:8926967"
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                     WGSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNADNPSMNFNVVSCPSELIAKTNCR
                     RN"
BASE COUNT      202 a    153 c    210 g    219 t
ORIGIN

  Query Match           19.5%;  Score 198.8;  DB 3;  Length 784;
  Best Local Similarity   60.8%;  Pred. No. 1.2e-44;
  Matches  383;  Conservative    0;  Mismatches  232;  Indels   15;  Gaps    3;

Qy        390 TGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGG 449
              ||  |  ||    || || || |||||||| || || || |  |||||| |||||   |
Db         72 TGACAGTGGCAAAACAACGCGCTATTGGGACTGTTGCAAAGGGTCCTGTGGCTGGGAAGC 131

Qy        450 TAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT-- 507
              |||||| |||| ||   ||  |  |  | ||    ||||||||   |||     ||
Db        132 AAAGGCCGATGTTAGCAAGCCCATTGACACATGCGCGAAAGATGGGACCACCAGAGTTGC 191

Qy        508 -AGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAA 566
               ||  ||  ||  |   |||||| ||| | || ||  || | ||||||||  | ||  |
Db        192 AAGCAACGACACCGTGAAAAGTGGTTGTGATGGCGGGGACGGATACATGTGCTATGATCA 251

Qy        567 CCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGG 626
              |||  |||| ||| || ||      ||||  ||| || |||||||| || ||   |
Db        252 AACACCGTGGGGTGTTAATGATTCATATGCCCTTGGCTTTGCTGCTGCAGCAAT---TTC 308

Qy        627 TGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGT 686
              || ||| |||      |  |||||    |||| ||||||||| ||||| ||| | | ||
Db        309 AGGAGGCGAAAAGGCCGCATGCTGCAACTGTTACGAACTTACGTTCACCTCTGGCCCCGT 368

Qy        687 TGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTAC 746
              |||  |||||||||  ||| || || || |||||||| || ||   | || |||
Db        369 CAATGGCAAGAAGATGACTGTGCAGGTTACCAACACTGGAGGCGACTTGGGTTCC----- 423

Qy        747 TGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGTTC 806
                 || |||||  |    || || ||||| || ||||| |||| |||||  || |
Db        424 ----AACCAATTTGATCTTGCCATACCTGGTGGCGGAGTTGGAATTTATAATGGATGCAC 479

Qy        807 CAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCTGC 866
              || |  |||||||||    || || |||||     | || || ||  |||| |||
Db        480 AGCTCAGTCTGGTGCTCCTGCCGATGGGTGGGGAAGTCGGTATGGAGGGGTTTCCTCTCG 539

Qy        867 ATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTG 926
              || ||||||   |||||||| |  || |||||||| ||  | ||||||||  | ||
Db        540 CAGCGAATGCTCTCAACTTCCTTCAGGTCTTCAAGCTGGCTGCCAGTGGAGATTTGATTG 599

Qy        927 GTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTAAGGAAAT 986
              ||||  | || || || ||  |||||  | ||| |  ||  | || || ||  |  |
Db        600 GTTCCAAAATGCCGACAATCCGTCCATGAACTTCAACGTCGTGTCGTGCCCCAGCGAGTT 659

Qy        987 CACCGCCAAGACAGGTTGTTCAAGAAAATA 1016
              |  || || ||   |||  | | || ||
Db        660 GATTGCGAAAACCAATTGCAGACGCAATTA 689


RESULT 8
AB045165
LOCUS       AB045165                781 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:2-54, complete cds.
ACCESSION   AB045165
VERSION     AB045165.1  GI:8926962
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:2-54.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 781)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
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                     /clone="2-54"
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                     /protein_id="BAA98035.1"
                     /db_xref="GI:8926963"
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                     WGSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNADNPSINFNVVSCPGELIANTNCR
                     RN"
BASE COUNT      193 a    143 c    210 g    235 t
ORIGIN

  Query Match           19.3%;  Score 196.4;  DB 3;  Length 781;
  Best Local Similarity   61.0%;  Pred. No. 5.6e-44;
  Matches  377;  Conservative    0;  Mismatches  226;  Indels   15;  Gaps    3;

Qy        403 ACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTC 462
              || || || || |||||||||| || |    ||| | |||   |  |||||  ||||
Db         82 ACAACCCGGTACTGGGATTGCTGCAAAGGAAGTTGTGGGTGGGAAGCAAAGGCTGATGTA 141

Qy        463 AGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT---AGTGACAGCAAT 519
              ||    ||| |  |  | |||   ||||||||     ||     ||  ||| ||   |
Db        142 AGCAAGCCTATTGATACATGTGCGAAAGATGGCACAACAAGAGTTGCAAGTAACGATACG 201

Qy        520 GCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAACCTTGGGCT 579
              |    ||    |||||  |  | |||||||||  | ||  |    ||| | |||
Db        202 GTTAAATCCGGCTGTGATGGTGGAGAAGGATACATGTGTTATGATCAAACGCCTCGTGCT 261

Qy        580 GTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGTGGTGGTGAATCT 639
              || || ||      ||||  ||| ||||| ||||| || |||   || || |   | ||
Db        262 GTCAATGATTCTTATGCCATTGGCTTCGCCGCTGCGGCTATCTCAGGAGGAGAGAAGGCT 321

Qy        640 CGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAG 699
              || |||      |||| |||| | |||||||| ||     | ||   ||| ||||||
Db        322 GCTTGTTGC---CAGTGTTACGAATTGACTTTCACCTCGGGACCGGTGAATGGAAAGAAG 378

Qy        700 ATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTT 759
              |||  ||| ||||| |||||||||||| || |||||||| |||          ||| |||
Db        379 ATGACTGTTCAAGTTACTAACACTGGGGGCGATCTTGGTTCC---------AACCAGTTT 429

Qy        760 GACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGTTCCAGCCAATGGGGT 819
              ||  |    || || || |||||||| || || |  ||||| ||  ||   |||| |||
Db        430 GATCTTGCTATTCCAGGGGGTGGTGTGGGAATATATAATGGATGCACCGCTCAATCTGGT 489

Qy        820 GCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCTGCATCTGACTGCTCT 879
              |||||   || || |||||      |||| || ||| |||| |||     ||| || ||
Db        490 GCTCCTGCAGATGGATGGGGAAGCCGATATGGCGGTGTTTCCTCTCGTAGTGAATGTTCC 549

Qy        880 AGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCT 939
              |||||  || |  ||  || ||||| ||  | ||| |||  | ||||| | || ||
Db        550 CAGCTTCCATCAGGTCTTCAGGCTGGATGCCAGTGGCGATTTGATTGGTTCCAAAATGCA 609

Qy        940 GATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTAAGGAAATCACCGCCAAGACA 999
              |||||  ||    ||| |  | ||| |  ||  | || |||   ||| | |  ||||| ||
Db        610 GATAATCCGTCCATCAACTTCAACGTCGTATCGTGCCCTGGTGAACTGATTGCCAACACC 669
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Qy       1000 GGTTGTTCAAGAAAATAA 1017
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Db        670 AATTGCAGACGTAATTAA 687
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RESULT 9
AB045177
LOCUS AB045177 785 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:1-14, complete cds.
ACCESSION AB045177
VERSION AB045177.1 GI:8926986
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:1-14.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
JOURNAL Extremophiles 4 (6), 343-349 (2000)
MEDLINE 21020023
REFERENCE 2 (bases 1 to 785)
AUTHORS Ohkuma,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
FEATURES Location/Qualifiers
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/organism="Reticulitermes speratus hindgut symbiont 130484"
/clone="1-14"
CDS 27. .686
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/db_xref="GI:8926987"
/translation="MLFYILTFVGLSLAESGKTTRYWDCCKGSCGWEKKANVDKPIDT
CAKDGTTRVASNDTVKSGCDGGEGYMCYDQTPWSVNDSYSYGFAAAACCGGESGACCG
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GSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNADNPNINFSSVRCPAEIIAKTNCNR
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BASE COUNT 217 a 133 c 214 g 221 t
ORIGIN

Query Match 19.2%; Score 194.8; DB 3; Length 785;
Best Local Similarity 60.8%; Pred. No. 1.6e-43;
Matches 376; Conservative 0; Mismatches 227; Indels 15; Gaps 3;

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Qy        403 ACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTC 462
              || ||||| |||||||||||||| || |    |||| | |||     ||||||||||
Db         81 ACAACTCGCTATTGGGATTGCTGCAAAGGAAGCTGTGGGTGGGAAAAGAAGGCCAATGTG 140

Qy        463 AGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT---AGTGACAGCAAT 519
                  ||  |  |  | |||   || |||||   |||      |    ||  | . ||
Db        141 GACAAACCCATTGATACATGTGCAAAGGATGGCACCACCAGAGTGGCAAGCAATGACACA 200

Qy        520 GCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAACCTTGGGCT 579
              | | |   ||| ||| | |||||  |  | ||||||||  | ||  |    || |||  |
Db        201 GTCAAGTCTGGTTGTGATGGTGGAGAGGGGTACATGTGCTATGATCAGACGCCATGGAGT 260

Qy        580 GTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGTGGTGGTGAATCT 639
              |||||  |||     | | || |||||  |||||||| ||     |  |||| |||||   |
Db        261 GTAAATGACTCGTATTCATACGGTTTTGCTGCTGCAGC---TTGCTGTGGCGGTGAGAGT 317

Qy        640 CGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAG 699
                |    ||||||   || |  ||  | || |||||   |    | ||    || ||| |
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Db        318 GGTGCTTGCTGTGGCTGCTATGATTTGACATTCACAAGTGGGCCGGTCAACGGAAAGCAT 377

Qy        700 ATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTT 759
              ||| |||| ||| | || ||||| || |||||||| ||||||          ||| |||
Db        378 ATGATTGTTCAAATAACGAACACAGGGGGTGATCTAGGCTCC---------AATCAATTT 428

Qy        760 GACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGTTCCAGCCAATGGGGT 819
              ||  |    || || |||||||| || || |||| ||| || ||  |   ||||| ||||
Db        429 GATCTTGCCATTCCGGGTGGTGGGGTCGGAATTTACAACGGATGCACGGCCCAATCGGGT 488

Qy        820 GCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCTGCATCTGACTGCTCT 879
              |||||    || ||||||||     | || || ||| |||| ||   |  ||| ||||||
Db        489 GCTCCTTCAGATGGTTGGGGAAGCCGGTATGGAGGTGTTTCATCAAGAAGTGAATGCTCT 548

Qy        880 AGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCT 939
                |||||  || | ||| || ||||| ||  | ||||||||  | ||||||  ||||||||
Db        549 CAGCTTCCATCAGGACTGCAGGCTGGATGCCAGTGGAGATTTGATTGGTTCCAGAACGCT 608

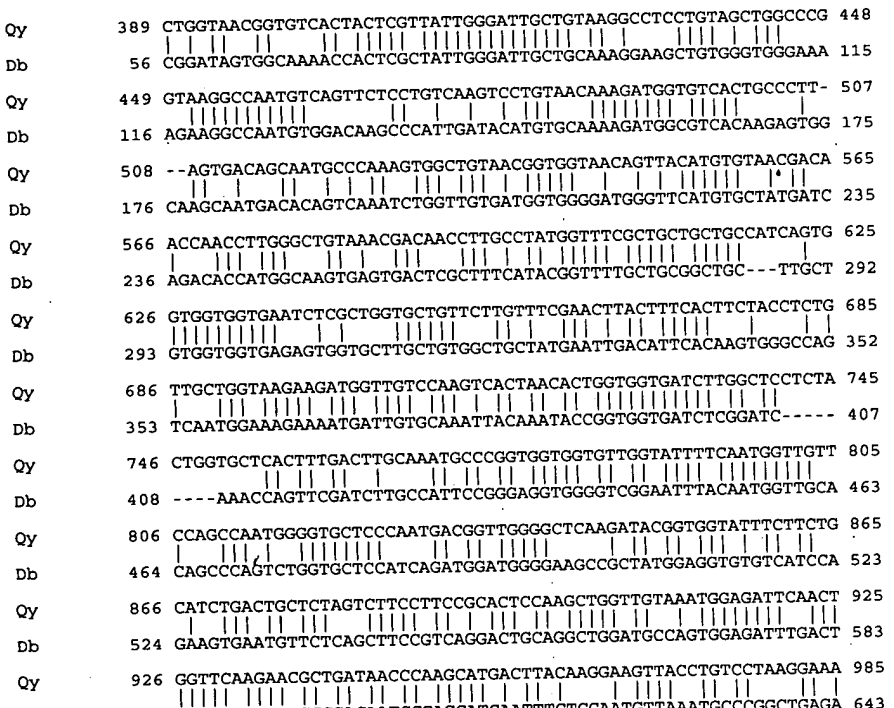
Qy        940 GATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTAAGGAAATCACCGCCAAGACA 999
              || || || | ||| | || ||      ||||  || ||    || || |  ||||| ||
Db        609 GACAATCCGAACATCAATTTCAGCAGTGTTAGATGCCCAGCTGAGATTATTGCCAAAACC 668

Qy       1000 GGTTGTTCAAGAAAATAA 1017
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Db        669 AATTGCAACCGAGTTTAA 686
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RESULT 10
AB045174
LOCUS AB045174 759 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:B1-1, complete cds.
ACCESSION AB045174
VERSION AB045174.1 GI:8926980
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:B1-1.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
JOURNAL Extremophiles 4 (6), 343-349 (2000)
MEDLINE 21020023
REFERENCE 2 (bases 1 to 759)
AUTHORS Ohkuma,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
FEATURES Location/Qualifiers
source 1. .759
/organism="Reticulitermes speratus hindgut symbiont 130484"
/clone="B1-1"
CDS 16. .675
/codon_start=1
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/protein_id="BAA98044.1"
/db_xref="GI:8926981"
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CAKDGVTRVASNDTVKSGCDGGDGFMCYDQTPWQVSDSLSYGFAAAACCGGESGACCG
CYELTFTSGPVNGKKMIVQITNTGGDLGSNQFDLAIPGGGVGIYNGCTAQSGAPSDGW
GSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNADNPSINFSNVKCPAEIIAKTNCNR
V"
BASE COUNT 194 a 133 c 208 g 224 t
ORIGIN

Query Match 19.1%; Score 194.4; DB 3; Length 759;

Best Local Similarity 60.3%; Pred. No. 2e-43;
Matches 381; Conservative 0; Mismatches 236; Indels 15; Gaps 3;



RESULT 11
AB045173
LOCUS AB045173 783 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:7-10, complete cds.
ACCESSION AB045173
VERSION AB045173.1 GI:8926978
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:7-10.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
JOURNAL Extremophiles 4 (6), 343-349 (2000)
MEDLINE 21020023
REFERENCE 2 (bases 1 to 783)
AUTHORS Ohkuma,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES Location/Qualifiers
source 1. .783
/organism="Reticulitermes speratus hindgut symbiont 130484"
/clone="7-10"
CDS 34. .693
/codon_start=1
/product="family 45 cellulase homologue"
/protein_id="BAA98043.1"
/db_xref="GI:8926979"
/translation="MLLYILTFIGLSLADSGKTTRYWDCCKGSCGWEKKANVDKPIDT CAKDGTTRVASNDTVKSGCDGGTGFMCYDQTPWQVSDSLSYGFAAAACCGGESGACCG CYELTFTSGPVNGKKMIVQITNTGGDLGSNQFDLAIPGGGVGIYNGCTAQSGAPSDGW GSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNADNPSINFSNVKCPSEIIAKTNCNR V"
BASE COUNT 201 a 150 c 209 g 223 t
ORIGIN

Query Match 18.9%; Score 192.6; DB 3; Length 783;
Best Local Similarity 60.6%; Pred. No. 6.5e-43;
Matches 375; Conservative 0; Mismatches 229; Indels 15; Gaps 3;



RESULT 12
AB045176
LOCUS AB045176 802 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45

```
          cellulase homologue, clone:1-16, complete cds.
ACCESSION   AB045176
VERSION     AB045176.1  GI:8926984
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:1-16.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites) .
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 802)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
     source          1. .802
                     /organism="Reticulitermes speratus hindgut symbiont
                     130484"
                     /clone="1-16"
     CDS             60. .719
                     /codon_start=1
                     /product="family 45 cellulase homologue"
                     /protein_id="BAA98046.1"
                     /db_xref="GI:8926985"
                     /translation="MLLYILAFISWSLADSGRTTRYWDCCKGSCGWEKKANVDKPIDT
                     CAKDGTTRVASNDTVKSGCDGGDGFMCYDQTPWQVSDSLSYGFAAAACCGGESGACCG
                     CYELTFTSGPVNGKKMVVQITNTGGDLGSNQFDLAIPGGGVGIYNGCTAQSGAPSDGW
                     GSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNADNPSINFSQVSCPSEIIAKTHCNR
                     V"
BASE COUNT      195 a    155 c    219 g    233 t
ORIGIN
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Query Match 18.8%; Score 191.2; DB 3; Length 802;
Best Local Similarity 60.0%; Pred. No. 1.6e-42;
Matches 379; Conservative 0; Mismatches 238; Indels 15; Gaps 3;

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Qy        389 CTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCG 448
Db        100 CTGACAGTGGTAGAACCACCCGCTATTGGGACTGCTGCAAAGGAAGCTGTGGGTGGGAAA 159

Qy        449 GTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTT- 507
Db        160 AGAAGGCCAATGTGGACAAGCCCATTGATACATGTGCAAAAGATGGGACCACGAGAGTTG 219

Qy        508 --AGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACA 565
Db        220 CAAGCAATGACACAGTCAAGTCTGGTTGTGATGGTGGGGACGGGTTCATGTGCTATGACC 279

Qy        566 ACCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTG 625
Db        280 AGACACCATGGCAAGTGAGTGACTCGCTTTCATACGGTTTTGCTGCGGCTGC---TTGCT 336

Qy        626 GTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTG 685
Db        337 GTGGTGGTGAGAGTGGTGCTTGCTGTGGCTGCTATGAATTGACATTCACAAGTGGGCCGG 396

Qy        686 TTGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTA 745
Db        397 TTAACGGAAAGAAAATGGTTGTGCAAATTACAAATACCGGTGGTGATCTCGGATC----- 451

Qy        746 CTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGTT 805
Db        452 ----AAACCAGTTCGATCTTGCCATTCCGGGAGGTGGGGTCGGAATTTACAACGGTTGCA 507

Qy        806 CCAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTTCTTCTG 865
Db        508 CAGCCCAGTCTGGTGCTCCATCAGATGGGTGGGGAAGCCGCTATGGAGGTGTGTCATCCA 567

Qy        866 CATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACT 925
Db        568 GAAGTGAATGTTCTCAGCTTCCATCAGGACTGCAGGCTGGATGCCAGTGGAGATTTGACT 627

Qy        926 GGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTAAGGAAA 985
Db        628 GGTTCCAGAATGCCGACAATCCGTCGATCAATTTCTCCCAAGTTAGCTGCCCGTCTGAGA 687

Qy        986 TCACCGCCAAGACAGGTTGTTCAAGAAAATAA 1017
Db        688 TTATTGCCAAAACCCATTGCAACCGAGTTTAA 719
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RESULT 13
FSOKCH
LOCUS       FSOKCH                  1443 bp    mRNA    linear   PLN 28-APR-1995
DEFINITION  Fusarium oxysporum K-family cellulase homologue mRNA, complete cds.
ACCESSION   L29381
VERSION     L29381.1  GI:520822
KEYWORDS    K-family cellulase homologue; cellulase; homologue.
SOURCE      Fusarium oxysporum cDNA to mRNA.
  ORGANISM  Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1  (bases 1 to 1443)
  AUTHORS   Sheppard,P.O., Grant,F.J., Oort,P.J., Sprecher,C.A., Foster,D.C.,
            Hagen,F.S., Upshall,A., McKnight,G.L. and O'Hara,P.J.
  TITLE     The use of conserved cellulase family-specific sequences to clone
            cellulase homologue cDNAs from Fusarium oxysporum
  JOURNAL   Gene 150 (1), 163-167 (1994)
  MEDLINE   95047531
   PUBMED   7959045
FEATURES             Location/Qualifiers
     source          1. .1443
                     /organism="Fusarium oxysporum"
                     /db_xref="taxon:5507"
     CDS             83. .1213
                     /note="putative"
                     /codon_start=1
                     /product="K-family cellulase homologue"
                     /protein_id="AAA65589.1"
                     /db_xref="GI:520823"
                     /translation="MRSYTLLALAGPLAVSAASGSGHSTRYWDCCKPSCSWSGKAAVN
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                     ALGGAQYGGISSRSECDSYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDISG
                     CKRDDDSSFPAFKGDTSASKPQPSSSAKKTTSAAAAAQPQKTKDSAPVVQKSSTKPAA
                     QPEPTKPADKPQTDKPVATKPAATKPAQPVNKPKTTQKVRGTKTRGSCPAKTDATAKA
                     SVVPAYYQCGGSKSAYPNGNLACATGSKCVKQNEYYSQCVPN"
BASE COUNT      325 a    448 c    332 g    338 t
ORIGIN
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Query Match 18.6%; Score 189.4; DB 8; Length 1443;
Best Local Similarity 59.0%; Pred. No. 5.1e-42;
Matches 369; Conservative 0; Mismatches 241; Indels 15; Gaps 2;

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Qy        380 GTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTA 439
Db        129 GTGCTGCTTCTGGAAGCGGTCACTCTACTCGATACTGGGATTGCTGCAAGCCTTCTTGCT 188

Qy        440 GCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCA 499
Db        189 CTTGGAGCGGAAAGGCTGCTGTCAACGCCCCTGCTTTAACTTGTGATAAGAACGACAACC 248

Qy        500 CTGCCCTTAGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTA 559
Db        249 CCATTTCCAACACCAATGCTGTCAACGGTTGTGAGGGTGGTGGTTCTGCTTATGCTTGCA 308
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Qy        560 ACGACAACCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCA 619
Db        309 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGA 368

Qy        620 TCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTA 679
Db        369 TCTCCGGTGGCTCCGAGGCCAGCTGGTGCTGTGCTTGCTATGCTTTGACCTTCACCACTG 428

Qy        680 CCTCTGTTGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCT 739
Db        429 GCCCCGTCAAGGGCAAGAAGATGATCGTCCAGTCCACCAACACTGGAGGTGATCTCGGCG 488

Qy        740 CCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATG 799
Db        489 ACA---------ACCACTTCGATCTCATGATGCCCGGCGGTGGTGTCGGTATCTTCGACG 539

Qy        800 GTTGTTCCAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTT 859
Db        540 GCTGCACCTCTGAGTTCGG------CAAGGCTCTCGGCGGTGCCCAGTACGGCGGTATCT 593

Qy        860 CTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGAT 919
Db        594 CCTCCCGAAGCGAATGTGATAGCTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGAT 653

Qy        920 TCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTA 979
Db        654 TCGACTGGTTCGAGAACGCCGACAACCCTGACTTCACCTTTGAGCAGGTTCAGTGCCCCA 713

Qy        980 AGGAAATCACCGCCAAGACAGGTTG 1004
Db        714 AGGCTCTCCTCGACATCAGTGGATG 738
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RESULT 14
A21795
LOCUS A21795 1473 bp mRNA linear PAT 20-SEP-1995
DEFINITION F.oxysporum mRNA for endonuclease component.
ACCESSION A21795
VERSION A21795.1 GI:1246874
KEYWORDS .
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

FEATURES Location/Qualifiers
source 1. .1473
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/strain="DSM 2672"
/db_xref="taxon:5507"
CDS 97. .1227
/codon_start=1
/product="endonuclease"
/protein_id="CAA01575.1"
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ALGGAQYGGISSRSECDSYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDISG
CKRDDDSSFPAFKVDTSASKPQPSSSAKKTTSAAAAAQPQKTKDSAPVVQKSSTKPAA
QPEPTKPADKPQTDKPVATKPAATKPVQPVNKPKTTQKVRGTKTRGSCPAKTDATAKA
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BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 18.6%; Score 189.4; DB 6; Length 1473;
Best Local Similarity 59.0%; Pred. No. 5.1e-42;
Matches 369; Conservative 0; Mismatches 241; Indels 15; Gaps 2;

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Qy        380 GTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCTTGTA 439
Db        143 GTGCTGCTTCTGGAAGCGGTCACTCTACTCGATACTGGGATTGCTGCAAGCCTTCTTGCT 202

Qy        440 GCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCA 499
Db        203 CTTGGAGCGGAAAGGCTGCTGTCAACGCCCCTGCTTTAACTTGTGATAAGAACGACAACC 262

Qy        500 CTGCCCTTAGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTA 559
Db        263 CCATTTCCAACACCAATGCTGTCAACGGTTGTGAGGGTGGTGGTTCTGCTTATGCTTGCA 322

Qy        560 ACGACAACCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCA 619
Db        323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGA 382

Qy        620 TCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTA 679
Db        383 TCTCCGGTGGCTCCGAGGCCAGCTGGTGCTGTGCTTGCTATGCTTTGACCTTCACCACTG 442

Qy        680 CCTCTGTTGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCT 739
Db        443 GCCCCGTCAAGGGCAAGAAGATGATCGTCCAGTCCACCAACACTGGAGGTGATCTCGGCG 502

Qy        740 CCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATG 799
Db        503 ACA---------ACCACTTCGATCTCATGATGCCCGGCGGTGGTGTCGGTATCTTCGACG 553

Qy        800 GTTGTTCCAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTT 859
Db        554 GCTGCACCTCTGAGTTCGG------CAAGGCTCTCGGCGGTGCCCAGTACGGCGGTATCT 607

Qy        860 CTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGAT 919
Db        608 CCTCCCGAAGCGAATGTGATAGCTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGAT 667

Qy        920 TCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTA 979
Db        668 TCGACTGGTTCGAGAACGCCGACAACCCTGACTTCACCTTTGAGCAGGTTCAGTGCCCCA 727

Qy        980 AGGAAATCACCGCCAAGACAGGTTG 1004
Db        728 AGGCTCTCCTCGACATCAGTGGATG 752
```

RESULT 15
A23637
LOCUS A23637 1473 bp mRNA linear PAT 19-SEP-1995
DEFINITION F. oxysporum endoglucanase gene.
ACCESSION A23637
VERSION A23637.1 GI:832888
KEYWORDS endoglucanase.
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Convents,A.C., Busch,A. and Baeck,A.C.
TITLE Detergent compositions with high activity cellulase and softening clays
JOURNAL Patent: EP 0495258-A 3 22-JUL-1992;
THE PROCTER & GAMBLE COMPANY

FEATURES Location/Qualifiers
source 1. .1473
/organism="Fusarium oxysporum"
/db_xref="taxon:5507"
CDS 97. .1227
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/protein_id="CAA01682.1"
/db_xref="GI:832889"
/translation="MRSYTLLALAGPLAVSAASGSGHSTRYWDCCKPSCSWSGKAAVN
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ALGGAQYGGISSRSECDSYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDISG
CKRDDDSSFPAFKVDTSASKPQPSSSAKKTTSAAAAAQPQKTKDSAPVVQKSSTKPAA

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SVVPAYYQCGGSKSAYPNGNLACATGSKCVKQNEYYSQCVPN"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 18.6%; Score 189.4; DB 6; Length 1473;
Best Local Similarity 59.0%; Pred. No. 5.1e-42;
Matches 369; Conservative 0; Mismatches 241; Indels 15; Gaps 2;

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Qy        380 GTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTA 439
              ||| ||| ||||| | ||||  | ||||||| || ||||||||||| ||| | || ||
Db        143 GTGCTGCTTCTGGAAGCGGTCACTCTACTCGATACTGGGATTGCTGCAAGCCTTCTTGCT 202

Qy        440 GCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCA 499
                ||| ||| |||||  |||||  | ||||      | ||| | || | |    |
Db        203 CTTGGAGCGGAAAGGCTGCTGTCAACGCCCCTGCTTTAACTTGTGATAAGAACGACAACC 262

Qy        500 CTGCCCTTAGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTA 559
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Db        263 CCATTTCCAACACCAATGCTGTCAACGGTTGTGAGGGTGGTGGTTCTGCTTATGCTTGCA 322

Qy        560 ACGACAACCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCGCTGCTGCTGCCA 619
              | || ||   || |||||||| |||||  | |||||||| |||||||||||| |    |
Db        323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGA 382

Qy        620 TCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTA 679
              ||   |||||    ||  |  |||||||||| |||| |  |   | || |||||  ||
Db        383 TCTCCGGTGGCTCCGAGGCCAGCTGGTGCTGTGCTTGCTATGCTTTGACCTTCACCACTG 442

Qy        680 CCTCTGTTGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTGGTGATCTTGGCT 739
              | | ||    || |||||||| | |||||   ||| |||||||| |||||||| |||
Db        443 GCCCCGTCAAGGGCAAGAAGATGATCGTCCAGTCCACCAACACTGGAGGTGATCTCGGCG 502

Qy        740 CCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATG 799
              |          ||||| ||  |    |||||||| |||||||| |||||  ||| | |
Db        503 ACA---------ACCACTTCGATCTCATGATGCCCGGCGGTGGTGTCGGTATCTTCGACG 553

Qy        800 GTTGTTCCAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGATACGGTGGTATTT 859
              | || ||    | |  ||      ||| |      | ||  |   ||||| ||||| |
Db        554 GCTGCACCTCTGAGTTCGG------CAAGGCTCTCGGCGGTGCCCAGTACGGCGGTATCT 607

Qy        860 CTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGAT 919
              | ||   |  || ||  |||   ||       ||| | |  ||||| | ||| |||
Db        608 CCTCCCGAAGCGAATGTGATAGCTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGAT 667

Qy        920 TCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCTA 979
              || |||||||| ||||||| || |||||   | | || |   || | |||   || || |
Db        668 TCGACTGGTTCGAGAACGCCGACAACCCTGACTTCACCTTTGAGCAGGTTCAGTGCCCCA 727

Qy        980 AGGAAATCACCGCCAAGACAGGTTG 1004
              |||   ||  || ||  |  || ||
Db        728 AGGCTCTCCTCGACATCAGTGGATG 752
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